



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Duft, Bradford
Kolterman, Orville
- (ii) TITLE OF THE INVENTION: METHODS FOR TREATING OBESITY
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LYON & LYON
 - (B) STREET: 633 WEST FIFTH STREET, SUITE 4700
 - (C) CITY: LOS ANGELES
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/870,762
 - (B) FILING DATE: 06-JUN-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: DUFT, BRADFORD J
 - (B) REGISTRATION NUMBER: 32,219
 - (C) REFERENCE/DOCKET NUMBER: 226/104
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-552-8400
 - (B) TELEFAX: 619-552-0159
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
1 5 10 15
Leu Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr
20 25 30
Asn Val Gly Ser Asn Thr Tyr
35

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	Arg	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Pro	Thr
				20					25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	Arg	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Ser	Thr
				20					25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

- (B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Pro	Ser	Thr
				20					25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Val	Leu	Pro	Pro	Thr
				20					25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys	Asp	Asn	Thr	Ala	Thr	Lys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Ser	Ser	Thr
				20					25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Ser	Ser	Thr
				20					25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
1 5 10 15
Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr
20 25 30
Asn Val Gly Ser Asn Thr Tyr
35

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
1 5 10 15
Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr
20 25 30
Asn Val Gly Ser Asn Thr Tyr
35

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
1 5 10 15
Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Pro Thr
20 25 30
Asn Val Gly Ser Asn Thr Tyr
35

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Ser	Thr
				20					25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Ser	Thr
				20					25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15
Leu	Val	Arg	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Ser	Thr
			20						25					30
Asn	Val	Gly	Ser	Asn	Thr	Tyr								
				35										

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1				5					10					15

Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr
 20 25 30
 Asn Val Gly Ser Asn Thr Tyr
 35

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
 1 5 10 15
 Leu Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr
 20 25 30
 Asn Val Gly Ser Asn Thr Tyr
 35